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DR⁺protein - protein search, using sw model

Run on: November 9, 2002, 06:49:07 ; Search time 38 Seconds

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
(without alignments)
207.382 Million cell updates/sec

Title: Perfect score: US-09-895-298A-83

Sequence: 1 MMNFQPPSKAWRASQMMTFF.....HDCSDLRSLRSVQEGNPR 190

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 4

Total number of hits satisfying chosen parameters: 49917

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries
Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	3.7	115	1 SMS2_ONCMY	Q91194 oncorhynchus
2	7	3.7	136	1 YD717_SCCHO	014010 schizosacch
3	7	3.7	151	1 SSB_RAT	p28042 rattus norv
4	7	3.7	215	1 I012_MEJJA	060347 methanococc
5	7	3.7	241	1 YFB9_MEJJA	058984 methanococc
6	7	3.7	259	1 IF2C_GALSU	008810 galderia s
7	7	3.7	338	1 PHND_ECOLI	F16682 escherichia
8	7	3.7	500	1 YDGR_ECOLI	P77304 escherichia
9	7	3.7	550	1 SYM_CHLNU	09p107 chlamydia m
10	7	3.7	553	1 ASNB_ECOLI	F22106 escherichia
11	7	3.7	1176	1 NTR_NEUCR	P38681 neurospora
12	7	3.7	1410	1 PDRB_YEAST	P40550 saccharomyce
13	6	3.2	20	1 YPRB_SERINA	P22581 serratia ma
14	6	3.2	61	1 HSP_CHICK	P15340 gallus gall
15	6	3.2	65	1 VC33_CYAPKA	P48273 cyanophora
16	6	3.2	67	1 PSBLI_PORPU	P51325 porphyra pu
17	6	3.2	88	1 VG30_BPMD2	P064224 mycobacteri
18	6	3.2	106	1 GASA_ARATH	P46690 arabidopsis
19	6	3.2	112	1 KV2D_MOUSE	P01629 mus musculu
20	6	3.2	112	1 OLTG_MOUSE	060888 mus musculu
21	6	3.2	113	1 KY2E_MOUSE	p03976 mus musculu
22	6	3.2	113	1 R130_SPOR	P58375 sporoptera
23	6	3.2	114	1 R130_BRABE	P58374 brachistost
24	6	3.2	136	1 ACP1_CASGL	P93092 casuarina g
25	6	3.2	138	1 Y850_AQUPE	067017 aquilex aeo
26	6	3.2	139	1 Y46B_RHISH	P55458 rhizobium s
27	6	3.2	146	1 AR16_CAREEL	p91167 caenorhabdi
28	6	3.2	148	1 SSR_HUMAN	Q04837 homo sapien
29	6	3.2	149	1 Y919_MEJJA	Q58329 methanococc
30	6	3.2	157	1 XYS2_PSPPU	005092 pseudomonas
31	6	3.2	167	1 TELT_HUMAN	Q15273 homo sapien
32	6	3.2	167	1 TEIT_MOUSE	Q70548 mus musculu
33	6	3.2	170	1 YC66_MESV1	Q9muq8 mesostigma

ALIGNMENTS

RESULT 1	SMS2_ONCMY	STANDARD;	PRT;	115 AA.
RT	SMS2_ONCMY			
ID	091194;			
AC				
DR				
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Somatostatin II precursor [Contains: [Tyr7,Gly10]somatostatin-14]			
DE	[Tyr7,Gly10]somatostatin-14]			
OS	Oncohyrnchus mykiss (Rainbow trout) (Salmo gairdneri)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Butteleostei;			
OC	Practanthopterygii; Salmoniformes; Salmonidae; Oncohyrnchus.			
OX	NCBI_TAXID:8022;			
RN				
[1]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-95554921; PubMed-7628694;			
RA	Moore C.A., Kittilson J.D., Dahl S.K., Sheridan M.A.;			
RT	"Isolation and characterization of a cDNA encoding for preprosomatostatin containing [Tyr7, Gly10]-somatostatin-14 from the endocrine pancreas of rainbow trout, <i>Oncorhynchus mykiss</i> ."			
RT	RT			
RL	Gen. Comp. Endocrinol. 98:253-261(1995).			
CC	-I- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.			
CC	-I- SURCELLULAR LOCATION: Secreted.			
CC	-I- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.			
CC	-I- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-I- InterPro; IPR004250; Somatostatin.			
DR	EMBL; U32471; AAC59695.1; -			
DR	InterPro; IPR004250; Somatostatin.			
DR	PFAM; PF03002; Somatostatin.			
DR	PFAM; PF03002; Somatostatin.			
FT	KW Cleavage on pair of basic residues; Hormone; Signal; Multigene family.			
FT	SGNAL	1	18	
FT	POTENTIAL.			
FT	PROPER	19	87	
FT	PEPTIDE	88	115	
FT	PEPTIDE	102	115	
FT	PEPTIDE	102	115	
FT	DISULFID	104	115	
FT	BY SIMILARITY			
FT	P03976	115 AA;	12963 MW;	52055025FC6D91 CRC64;
SQ	SEQUENCE	115 AA;	12963 MW;	52055025FC6D91 CRC64;
Query	Match	3.7%	Score 7;	DB 1;
Best	Local Similarity	10.0%	Pred. No. 4.1;	Length 115;
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0;
QY	175 LDLRSRR 181			
DB	30 LDLRSRR 36			

OP501. A77

ID YDP7_SCBPO STANDARD: PRT; 136 AA.

AC 01010;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein C29A4.07 in chromosome I.

GN SPC29A4.07.

OS Schizosaccharomyces pombe (Fission yeast).

OC Schizosaccharomyces pombe; Schizosaccharomycetes; Schizosaccharomyces.

OC NCBI_TaxID=4396;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=72;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Connor R., Crönin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodges G., Hollroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jägels K., Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitzch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Gromoprez B., Weltjens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wanabutt R., Burnelle B., Goffreau A., Cadieu E., Dreano S., Gloux S., Lelauze V., Mottier S., Lucas M., Rochet M., Gaillardin C., Talleda V.A., Garzon A., Rhode G., RA Datta R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forssburg S.L., Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., RA Shpakovski G. V., Ussery D., Barrell B.G., Nurse P., RT "The genome sequence of Schizosaccharomyces pombe.", RL Nature 415:871-880(2002).

CC -----

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CC -----

CC DR EMBL; AF043635; AAC18063.1; JOINED.

CC DR EMBL; AF043630; AAC18063.1; JOINED.

CC DR EMBL; AF043631; AAC18063.1; JOINED.

CC DR EMBL; AF043632; AAC18063.1; JOINED.

CC DR EMBL; AF043633; AAC18063.1; JOINED.

CC DR EMBL; AF043634; AAC18063.1; JOINED.

CC DR PIR; S13264; S13264.

CC DR PIR; JN0569; JN0569.

CC DR HSSP; Q04837; 3ULL.

CC DR InterPro; IPR00024; SSB_protein.

CC DR PTan; PR00436; SSB; 1.

CC DR TIGRFAMS; TIGR0621; ssb; 1.

CC DR PROSITE; PS00735; SSB; 1.

CC DR PROSITE; PS00736; SSB; 1.

CC DR DNA-binding; DNA replication; Mitochondrion; Transit peptide.

CC FT TRANSIT 1 15 MITOCHONDRIUM.

CC FT CHAIN 17 151 SINGLE-STRANDED DNA-BINDING PROTEIN.

CC SQ SEQUENCE 151 AA; 17455 MW; B9CA830AB280DD6D9 CRC64;

Query Match 3.7%; Score 7; DB 1; Length 136;

Best Local Similarity 100.0%; Pred. No. 4.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 INFGKDK 131

SQ SEQUENCE 136 AA; 1582 MW; 52EA5A74C06C9FE1 CRC64;

Query Match 3.7%; Score 7; DB 1; Length 136;

Best Local Similarity 100.0%; Pred. No. 4.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 INFGKDK 46

RESULT 3

SSB_RAT STANDARD: PRT; 151 AA.

AC P28042;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 30-MAY-2002 (Rel. 39, Last annotation update)

DE Single-stranded DNA-binding protein, mitochondrial precursor (ML-SSB) (MCSSB) (P16).

GN SSBP1 OR SSBP2

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.

OC NCBITaxID=10116;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Liver;

RC MEDLINE=93246247; PubMed=8482537;

RA Tiranti V., Rocchi M., Didonato S., Zeviani M.; "Cloning of human and rat cDNAs encoding the mitochondrial single-stranded DNA-binding protein (SSB)."; Gene 126:219-225(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAINS=Sprague-Dawley;

RX MEDLINE=98278843; PubMed=9611270;

RA Gupta S., van Tuyle G.C.; "the gene and processed pseudogenes of the rat mitochondrial single-strand DNA-binding protein: structure and promoter strength analysis"; Gene 212:269-278(1998).

RL RN SEQUENCE OF 17-46.

RX MEDLINE=91054186; PubMed=2221914;

RA Hoke G.D., Pawco P.A., Ledwith B.J., van Tuyle G.C.; "Structural and functional studies of the rat mitochondrial single-strand DNA binding protein P16.";

RT Arch. Biochem. Biophys. 282:116-124(1990).

RT -1- FUNCTION: THIS PROTEIN BINDS PREFERENTIALLY AND COOPERATIVELY TO SS-DNA, PROBABLY INVOLVED IN MITOCHONDRIAL DNA REPLICATION.

RT -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

RT -1- SIMILARITY: BELONGS TO THE SSB FAMILY.

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CC -----

CC DR EMBL; M94557; AAA67315.1;

CC DR EMBL; AF043635; AAC18063.1;

CC DR EMBL; AF043630; AAC18063.1; JOINED.

CC DR EMBL; AF043631; AAC18063.1; JOINED.

CC DR EMBL; AF043632; AAC18063.1; JOINED.

CC DR EMBL; AF043633; AAC18063.1; JOINED.

CC DR EMBL; AF043634; AAC18063.1; JOINED.

CC DR PIR; S13264; S13264.

CC DR PIR; JN0569; JN0569.

CC DR HSSP; Q04837; 3ULL.

CC DR InterPro; IPR00024; SSB_protein.

CC DR PTan; PR00436; SSB; 1.

CC DR TIGRFAMS; TIGR0621; ssb; 1.

CC DR PROSITE; PS00735; SSB; 1.

CC DR PROSITE; PS00736; SSB; 1.

CC DR DNA-binding; DNA replication; Mitochondrion; Transit peptide.

CC FT TRANSIT 1 15 MITOCHONDRIUM.

CC FT CHAIN 17 151 SINGLE-STRANDED DNA-BINDING PROTEIN.

CC SQ SEQUENCE 151 AA; 17455 MW; B9CA830AB280DD6D9 CRC64;

Query Match 3.7%; Score 7; DB 1; Length 151;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 SSIVLER 157

Db 22 SSIVLER 28

RESULT 4

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 CC
 CC or send an email to license@isb-sib.ch).
 CC
 DR
 EMBL; X66698; CAA17239; 1; -.
 DR
 PIR; S36410; S36410.
 DR
 InterPro; IPR00795; EF_GTPbind.
 DR
 InterPro; IPR00118; IF2.
 DR
 Pfam; PF0009; GTP_EFTU; 1.
 DR
 PROSITE; PS01176; IF2; PARTIAL.
 DR
 Initiation Factor; Protein biosynthesis; GTP-binding; Chloroplast.
 FT DOMAIN 172 >259 G-DOMAIN.
 FT DOMAIN 180 187 GTP (BY SIMILARITY).
 FT NON_TER 259 259
 SEQUENCE 259 AA; 29746 MW; 803DC24390F42EBA CRC64;
 Query Match 3.7%; Score 7; DB 1; Length 259;
 Best local Similarity 100.0%; Pred. No. 8; 7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 134 LIRKLIK 140
 Db 189 LIRKLIK 195

RESULT 7
 PHND_ECOLI
 ID PHND_ECOLI STANDARD; PRT; 338 AA.
 AC P16682;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phosphonates-binding periplasmic protein precursor.
 GN PHND OR PSID OR BAI105.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia;
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91193228; PubMed=1840580;
 RA Makino K., Kim S., Shinagawa H., Amemura M., Nakata A.;
 RT "Molecular analysis of the cryptic and functional phn operons for
 phosphonate use in Escherichia coli K-12.";
 RL J. Bacteriol. 173:2665-2672(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=95334362; PubMed=7610040;
 RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 RA Blattner F.R.;
 RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
 region from 92.8 through 100 minutes";
 RL Nucleic Acids Res. 23:2105-2119(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=90170953; PubMed=2155230;
 RA Chen C.M., Ye Q.Z., Zhu Z., Wagner B.L., Walsh C.T.;
 RT "Molecular biology of carbon-phosphorus bond cleavage. Cloning and
 sequencing of the phn (psid) genes involved in alkylphosphonate
 uptake and C-P lyase activity in Escherichia coli K-12.";
 RL J. Biol. Chem. 265:4461-4471(1990).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC FOR ALKYLPHOSPHONATES.
 CC -!- SUBCELLULAR LOCATION: periplasmic (Potential).
 CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN K12.
 CC
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 RESULT 8
 YDGR_ECOLI
 ID YDGR_ECOLI STANDARD; PRT; 500 AA.
 AC P77304;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical transporter ydgr.
 GN YDGR OR B1634.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collard-Vides J., Glaser J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Nakada S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Moronura K., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
 RA Tagami H., Takeda J., Takeimoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RT DNA Res. 3:363-377(1996).
 RL
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS.
 CC
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 CC

OC Saccharomyctales; Saccharomyctaceae; Saccharomyces.

OR NCBI_TaxID=4932;

RN [1] SEQUENCE FROM N.A.

RC STRAIN-S288C / AB972;

RA Barrell, B.G.; Baddock, K.; Bankier, A.T.; Bowman, S.; Brown, D.;

RA Churcher, C.M.; Connor, R.; Copsey, T.; Dear, S.; Devin, K.; Fraser, A.;

RA Gentiles, S.; Hamlyn, N.; Hornsill, T.S.; Hunt, S.; Jarels, K.; Jones, M.;

RA Louis, E.; Lye, G.; Moule, S.; Moule, T.; Odell, C.; Pearson, D.;

RA Rajandream, M.A.; Riles, L.; Rowley, N.; Skelton, J.; Smith, V.;

RA Walsh, S.V.; Whitehead, S.;

RA Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

RN [2] IDENTIFICATION, AND SEQUENCE OF 1-10.

RN RP MEDLINE=93355421; PubMed=7629127;

RA Decottignies, A.; Lambert, L.; Catty, P.; Degand, H.; Epping, E.A.;

RA Moye-Rowley, W.S.; Balzi, E.; Goffreau, A.;

RA "Analysis of the SNO2, a new multidrug ATP

RT binding cassette transporter of the yeast plasma membrane.";

RT J. Biol. Chem. 270:18150-18157(1995).

CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.

CC -1- SUBCELLULAR LOCATION: Integral membrane Protein (potential).

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CC -----

RESULT 13
YPRB_SERMA
YPRB_SERMA
STANDARD; PRT; 20 AA.
ID YPRB_SERMA
AC P22581;
DT 01-AUG-1991 (Rel. 19, created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PROB 5' region (fragment).
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN
RP SEQUENCE FROM N.A.

[1] SEQUENCE FROM N.A.
RC STRAIN-SR41;
RX MEDLINE=9137315; PubMed=1851803;
RA Omori, K.; Suzuki, S.; Imai, Y.; Komatsubara, S.;
RT "Analysis of the Serratia marcescens probA operon and feedback
RT control of proline biosynthesis.";
RT J. Gen. Microbiol. 137:509-517(1991).

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DR EMBL; D9051; BAA1453.1; -.
DR EMBL; X53086; CAA37253.1; -.
DR PIR; S11643; S11643.
DR PIR; C49753; C49753.
KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 20 AA; 2248 MW; 4DD7773527674 CRC64;
FT RESULT 14
FT HSP_CHEK
ID HSP_CHEK
AC P15340; P02320;
DT 21-JUL-1986 (Rel. 01, created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sperm histone (Protein) (Gallus).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

[1] SEQUENCE FROM N.A.
RP MEDLINE=89308679; PubMed=2745455;
RA Oliva, R.; Dixon, G.H.;
RT "Chicken protamine genes are intronless. The complete genomic
RT sequence and organization of the two loci.";
RT J. Biol. Chem. 264:12472-12481(1989).
RL

[2] SEQUENCE OF 48-61 FROM N.A.
RP MEDLINE=88112514; PubMed=2892748;
RA Oliva, R.; Mequita, J.; Marquita, C.; Dixon, G.H.;
RT "Haplod expression of the rooster protamine mRNA in the postmeiotic
stages of spermatogenesis";
Dev. Biol. 125:332-340(1988).

Query Match Similarity 3.7%; Score 7; DB 1; Length 1410;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 FFFFLFLF 25
Db 494 FFFFLFLF 500

RN [3]
 RP SEQUENCE
 RC TISSUE-Sperm;
 RX MEDLINE-770575; PubMed-992941;
 RA Nakano M., Tobita T., Ando T.;
 RT "Studies on a protamine (galline) from fowl sperm. 3. The total amino acid sequence of intact galline molecule.,";
 RL Int. J. Pept. Protein Res. 8:565-578(1976).
 CC -1- FUNCTION: PROAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
 CC -1- CAUTION: REF. 3 SEQUENCE WAS VERY DIFFERENT FROM THAT OBTAINED BY REF 1 AND REF 2.

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CC

DR EMBL; U38713; AAA58721.1; -;
 DR EMBL; M28100; AAA78931.1; -;
 DR EMBL; M19078; AAA90491.1; ALT_SEQ.
 DR PIR; A02662; GACH;
 DR PIR; A34326; A34326.
 DR InterPro; IPR00221; protamine_P1.
 DR Pfam; PF00260; protamine_P1; 1.
 KW PROSITE; PS00048; PROTAMINE_P1; 1.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein; Phosphorylation.
 FT INIT_MER 0 . . 0
 FT MOD_RES 8 . . 8
 SEQUENCE 61 AA; 7986 MW; 191E27BD3A73AAA3 CRC64;
 PHOSPHORYLATION (POTENTIAL).
 Query Match 3.2%; Score 6; DB 1; Length 65;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 178 RSRSV 183
 |||||
 Db 39 RSRSV 44

RESULT 15

Y333_CYAP1 STANDARD; PRT; 65 AA.
 ID PA8273;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 7.6 kDa protein ycf33.
 GN YCF33.
 OS Cyanophora paradoxa.
 OC Eukaryota; Glaucoophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TAXID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RT Reith M.E., Munholland J.J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.,";
 RN Plant Mol. Biol. Rep. 13:333-335(1995).
 RL -1- TM: PHOSPHORYLATION IS A LIGHT DEPENDENT REACTION CATALYZED BY A MEMBRANE-BOUND KINASE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PSBH FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC

DR EMBL; U38804; AAC08211.1; -;
 DR InterPro; IPR001056; PS1_PsBh.
 DR Pfam; PF00737; PsBh; 1.
 DR ProDom; PD003584; PS1_PsBh; 1.
 KW Photosystem III; Phosphorylation; Chloroplast; Transmembrane.
 FT TRANSMEM 29 49 POTENTIAL.
 SQ SEQUENCE 67 AA; 7530 MW; 6CC4CA40D3619 CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
 RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa: the genetic complexity of a primitive plastid.,";
 RT (In) Schenk H.E.A., Harrmann R., Jeon K.W., Mueller N.E., Schwemmer W. (eds.); Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg (1997).
 RL -1- SIMILARITY: BELONGS TO THE YCF33 FAMILY.
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CC DR EMBL; U30821; AAA81285.1; -;
 KW Cyanelle; Hypothetical protein.
 SQ SEQUENCE 65 AA; 7635 MW; EAFFD0C8B6233CE3 CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 65;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 LIVLII 102
 |||||
 Db 40 LIVLII 45

RESULT 16

PSBh_PORPU STANDARD; PRT; 67 AA.
 ID PSBh_PORPU
 AC P01325;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Photosystem II 10 kDa phosphoprotein.
 GN PSBh.
 OS Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TAXID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RT Reith M.E., Munholland J.J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.,";
 RN Plant Mol. Biol. Rep. 13:333-335(1995).
 RL -1- TM: PHOSPHORYLATION IS A LIGHT DEPENDENT REACTION CATALYZED BY A MEMBRANE-BOUND KINASE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PSBH FAMILY.
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CC

DR EMBL; U38804; AAC08211.1; -;
 DR InterPro; IPR001056; PS1_PsBh.
 DR Pfam; PF00737; PsBh; 1.
 DR ProDom; PD003584; PS1_PsBh; 1.
 KW Photosystem III; Phosphorylation; Chloroplast; Transmembrane.
 FT TRANSMEM 29 49 POTENTIAL.
 SQ SEQUENCE 67 AA; 7530 MW; 6CC4CA40D3619 CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 SSLVLE 156
 ID VG30_BPMD2 STANDARD; PRT; 88 AA.
 AC 064224;
 DT 15-DEC-1998 (Rel. 37, created)
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Gene 30 protein (GP30).
 GN 30.
 OS Mycobacteriophage D29.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 unclassified Siphoviridae.
 OX NCBI_TAXID=28369;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9830035; PubMed=9636706;
 RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
 RT "Genome structure of mycobacteriophage D29: implications for phage
 evolution"; J. Mol. Biol. 279:143-164(1998).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF022214; AAC18471.1; -
 RP SEQUENCE 88 AA; 10391 MW; 52071AE676E59CE CRC64;
 SQ Query Match 3.2%; Score 6; DB 1; Length 88;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 117 IRLIHE 122
 DB 65 IRLIHE 70
 DR -----
 RESULT 18
 GAS4_ARATH STANDARD; PRT; 106 AA.
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gibberellin-regulated protein 4 precursor.
 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
 related to the tomato GAST1 gene.," Plant Mol. Biol. 27:743-752(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 17
 ID VG30_BPMD2 STANDARD; PRT; 88 AA.
 AC 064224;
 DT 15-DEC-1998 (Rel. 37, created)
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Gene 30 protein (GP30).
 GN 30.
 OS Mycobacteriophage D29.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 unclassified Siphoviridae.
 OX NCBI_TAXID=28369;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21016721; PubMed=11130714;
 RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsun A., Muraki A., Nakayama S.,
 RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Habermann K., Murray J., Johnson D., Ronning T., Nelson J.,
 RA Kirchoff K., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Stoenking T., Rodger A., Courtney L., Courtney W., Dante M.,
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latrelle P.,
 RA Leonard S., Meyer R., Mulvane E., Ozersky P., Riley A., Strome C.,
 RA Wagner-McPhereson C., Wollam A., Yeakum M., Bell M., Dediha N.,
 RA Parnell L., Shan R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kirchoff K., Roth K., King L., Bahret A., Miller B., Marra M.,
 RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
 RA Langham S.-A., McCullagh B., Robben J., Grymonpre B., Zimmermann W.,
 RA Rampsperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirksen P., Moelijn P., Klein Lankhorst R.,
 RA Weltzieneger T., Botha G., Rose M., Hauf J., Berneiser S., Hempel S.,
 RA Feldpausch M., Lambertz S., Villarroel R., GieLEN J., Ardiles W.,
 RA Bentz O., Lemcke K., Kolesov R., Mayer K.F.W., Rudd S., Schoof H.,
 RA Schueler C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.,
 RA "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 thaliana.," RT Nature 408:823-826(2000).
 RL [4]
 RP SEQUENCE FROM N.A.
 RP -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gibberellin-regulated protein 4 precursor.
 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
 related to the tomato GAST1 gene.," Plant Mol. Biol. 27:743-752(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
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 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
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 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
 related to the tomato GAST1 gene.," Plant Mol. Biol. 27:743-752(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
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 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
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 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
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 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
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 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
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 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
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 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
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 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
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 GN GAS4 OR AT5G1523 OR FBK21_120.
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 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
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 RE RESULT 18
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 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
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 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gibberellin-regulated protein 4 precursor.
 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
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 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
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 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
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 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gibberellin-regulated protein 4 precursor.
 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
 related to the tomato GAST1 gene.," Plant Mol. Biol. 27:743-752(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gibberellin-regulated protein 4 precursor.
 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
 related to the tomato GAST1 gene.," Plant Mol. Biol. 27:743-752(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gibberellin-regulated protein 4 precursor.
 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
 related to the tomato GAST1 gene.," Plant Mol. Biol. 27:743-752(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gibberellin-regulated protein 4 precursor.
 GN GAS4 OR AT5G1523 OR FBK21_120.
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 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
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 OX NCBI_TAXID=3702;
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 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=7727751;
 RA Herzog M., Dorne A.-M., Greillet F.;
 RT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
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 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
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 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
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 RP SEQUENCE FROM N.A.
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 RE RESULT 18
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 AC P46650; Q49593;
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 DT 15-JUN-2002 (Rel. 41, Last sequence update)
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 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
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 OX NCBI_TAXID=3702;
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 RX STRAIN=CV_C24; TISSUE=Flower buds;
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 RN [2]
 RP SEQUENCE FROM N.A.
 MEDLINE=98179101; PubMed=9520278;
 RX Aubert D., Chevillard M., Dorne A.-M., Arlaud G., Herzog M.;
 RT -----
 RE RESULT 18
 ID GAS4_ARATH STANDARD; PRT; 106 AA.
 AC P46650; Q49593;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
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 GN GAS4 OR AT5G1523 OR FBK21_120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV_C24; TISSUE=Flower buds;
 MEDLINE=95244835; PubMed=77277

QY 95 LTILIVL 100
 ID KV2D_MOUSE STANDARD; PRT; 112 AA.
 AC P01629;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tg kappa chain V-II region 2S1.3.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83055101; PubMed=7141411;
 RA Herbst H., Chang J.Y., Aebersold R., Braun D.G.;
 RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
 the group A streptococcal polysaccharide."
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOClonal
 CC ANTIBODY AGAINST THE STREPTOCOCAL GROUP A POLYSACCHARIDE.
 DR HSSP; A01911; KVMS17.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM0046; IgV; 1.
 KW Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 112 112 SEQUENCE 112 AA; 12221 MW; BD5EF5E6D/89FBEC CRC64;
 QY 102 ITYLYW 107
 DB 35 ITYLYW 40
 RESULT 20
 ID OI7G_MOUSE STANDARD; PRT; 112 AA.
 AC Q60888;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Olfactory receptor 7G (M31) (Fragment).
 GN OLFR7.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J;
 RX MEDLINE=96149403; PubMed=8570653;
 RA S.L., Adamson M.C., Reissler K.J., Kozak C.A., Buck L.B.;
 RT "the chromosomal distribution of mouse odorant receptor genes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:884-888(1996).
 RESULT 19
 ID KV2D_MOUSE STANDARD; PRT; 112 AA.
 AC P01629;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tg kappa chain V-II region 2S1.3.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83055101; PubMed=7141411;
 RA Herbst H., Chang J.Y., Aebersold R., Braun D.G.;
 RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
 the group A streptococcal polysaccharide."
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOClonal
 CC ANTIBODY AGAINST THE STREPTOCOCAL GROUP A POLYSACCHARIDE.
 DR HSSP; A01911; KVMS17.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM0046; IgV; 1.
 KW Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 112 112 SEQUENCE 112 AA; 12221 MW; BD5EF5E6D/89FBEC CRC64;
 QY 91 FFFILT 96
 DB 84 FFFILT 89
 RESULT 21
 ID KV2E_MOUSE STANDARD; PRT; 113 AA.
 AC P03976;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region 17S9.1.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Hybridoma;
 RX MEDLINE=8512896B; PubMed=641768;
 RA Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
 RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C7B1/5
 group A-streptococcal polysaccharide."
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
 CC -1- MISCELLANEOUS: ANTI-STREPTOCOCAL GROUP A CARBOHYDRATE ANTIBODY.
 DR HSSP; A01912; KVMS17.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM0046; IgV; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.

DR HESP; P02901; 1ACP.
 DR Interpro; IPR03231; Acyl_carrier.
 DR Interpro; IPR00380; Ppantne_attach.
 DR Pfam; PPF00550; PP-binding; 1.
 DR PRODOM; PD00887; Acyl_carrier; 1.
 DR TIGRFAMS; TIGR00317; Acyl_carrier; 1.
 DR PROSITE; PS0075; ACP_DOMAIN; 1.
 DR PROSITE; PS0012; PHOSPHOPANTETHINE; 1.
 KW Fatty acid biosynthesis; Phosphopantethine; chloroplast;
 KW transit peptide; Multigene family.
 FT TRANSIT 1 52 CHLOROPLAST (POTENTIAL).
 FT CHAIN 53 136 ACTYL CARRIER PROTEIN 1.
 FT BINDING 91 91 PHOSPHOPANTETHINE (BY SIMILARITY).
 SQ SEQUENCE 136 AA; 14351 MW; 8DF68F53079414FB CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Result 25
 Y55_AQAE STANDARD PRT; 138 AA.
 AC ID [|||||]
 AC 067017; 16-OCT-2001 (Rel. 40, Created)
 AC 126 LIEKLI 131
 DB 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein AQ_850.
 GN AQ_850.
 OS Aquifex_aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex; AQEBI_TAXID=63363;
 OX AQEBI_TAXID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FT5;
 RX MEDLINE=98106666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Riedl R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RL Nature 392:353-358(1998).
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 CC -----
 CC -----
 DR EMBL; AE000710; AAC06980.1; -
 KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.
 FT TRANSMEM 11 POTENTIAL.
 SQ SEQUENCE 138 AA; 16457 MW; 7836DA14FC9C5F5 CRC44;
 Query Match 3.2%; Score 6; DB 1; Length 138;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Result 25
 AR16_CABEL STANDARD PRT; 146 AA.
 AC ID AR16_CABEL
 AC P01167;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable ARP2/3 complex 16 kDa subunit (P16-ARC).
 GN C46H11.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderae; Caenorhabditis.
 OX AQEBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Miller N., Bradshtad H., Wansley P.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 CC -1 - FUNCTION: PART OF A COMPLEX IMPLICATED IN THE CONTROL OF ACTIN
 CC POLYMERIZATION IN CELLS (BY SIMILARITY).
 CC -1 - SUBUNIT: BELONGS TO A COMPLEX COMPOSED OF ARP2, ARP3, P41-ARC,
 CC P34-ARC, P21-ARC, P20-ARC AND P16-ARC (BY SIMILARITY).
 CC -1 - SIMILARITY: BELONGS TO THE ARP25 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR HESP; P02901; 1ACP.
 DR Interpro; IPR03231; Acyl_carrier.
 DR Interpro; IPR00380; Ppantne_attach.
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 FT TRANSIT 1 52 CHLOROPLAST (POTENTIAL).
 FT CHAIN 53 136 ACTYL CARRIER PROTEIN 1.
 FT BINDING 91 91 PHOSPHOPANTETHINE (BY SIMILARITY).
 SQ SEQUENCE 136 AA; 14351 MW; 8DF68F53079414FB CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 58;
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 AC ID [|||||]
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 AC 126 LIEKLI 131
 DB 16-OCT-2001 (Rel. 40, Last sequence update)
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 RA Riedl R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
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 DR Interpro; IPR03231; Acyl_carrier.
 DR Interpro; IPR00380; Ppantne_attach.
 DR Pfam; PPF00550; PP-binding; 1.
 DR PRODOM; PD00887; Acyl_carrier; 1.
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 FT CHAIN 53 136 ACTYL CARRIER PROTEIN 1.
 FT BINDING 91 91 PHOSPHOPANTETHINE (BY SIMILARITY).
 SQ SEQUENCE 136 AA; 14351 MW; 8DF68F53079414FB CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Result 25
 Y55_AQAE STANDARD PRT; 138 AA.
 AC ID [|||||]
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 AC 126 LIEKLI 131
 DB 16-OCT-2001 (Rel. 40, Last sequence update)
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 RT "The complete genome of the hyperthermophilic bacterium Aquifex
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 CC -----
 DR HESP; P02901; 1ACP.
 DR Interpro; IPR03231; Acyl_carrier.
 DR Interpro; IPR00380; Ppantne_attach.
 DR Pfam; PPF00550; PP-binding; 1.
 DR PRODOM; PD00887; Acyl_carrier; 1.
 DR TIGRFAMS; TIGR00317; Acyl_carrier; 1.
 DR PROSITE; PS0075; ACP_DOMAIN; 1.
 DR PROSITE; PS0012; PHOSPHOPANTETHINE; 1.
 KW Fatty acid biosynthesis; Phosphopantethine; chloroplast;
 KW transit peptide; Multigene family.
 FT TRANSIT 1 52 CHLOROPLAST (POTENTIAL).
 FT CHAIN 53 136 ACTYL CARRIER PROTEIN 1.
 FT BINDING 91 91 PHOSPHOPANTETHINE (BY SIMILARITY).
 SQ SEQUENCE 136 AA; 14351 MW; 8DF68F53079414FB CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Result 25
 Y55_AQAE STANDARD PRT; 138 AA.
 AC ID [|||||]
 AC 067017; 16-OCT-2001 (Rel. 40, Created)
 AC 126 LIEKLI 131
 DB 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein AQ_850.
 GN AQ_850.
 OS Aquifex_aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex; AQEBI_TAXID=63363;
 OX AQEBI_TAXID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FT5;
 RX MEDLINE=98106666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Riedl R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RL Nature 392:353-358(1998).
 CC -----
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 CC -----
 DR HESP; P02901; 1ACP.
 DR Interpro; IPR03231; Acyl_carrier.
 DR Interpro; IPR00380; Ppantne_attach.
 DR Pfam; PPF00550; PP-binding; 1.
 DR PRODOM; PD00887; Acyl_carrier; 1.
 DR TIGRFAMS; TIGR00317; Acyl_carrier; 1.
 DR PROSITE; PS0075; ACP_DOMAIN; 1.
 DR PROSITE; PS0012; PHOSPHOPANTETHINE; 1.
 KW Fatty acid biosynthesis; Phosphopantethine; chloroplast;
 KW transit peptide; Multigene family.
 FT TRANSIT 1 52 CHLOROPLAST (POTENTIAL).
 FT CHAIN 53 136 ACTYL CARRIER PROTEIN 1.
 FT BINDING 91 91 PHOSPHOPANTETHINE (BY SIMILARITY).
 SQ SEQUENCE 136 AA; 14351 MW; 8DF68F53079414FB CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Result 25
 Y55_AQAE STANDARD PRT; 138 AA.
 AC ID [|||||]
 AC 067017; 16-OCT-2001 (Rel. 40, Created)
 AC 126 LIEKLI 131
 DB 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein AQ_850.
 GN AQ_850.
 OS Aquifex_aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex; AQEBI_TAXID=63363;
 OX AQEBI_TAXID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FT5;
 RX MEDLINE=98106666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Riedl R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RL Nature 392:353-358(1998).
 CC -----
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 CC -----
 DR HESP; P02901; 1ACP.
 DR Interpro; IPR03231; Acyl_carrier.
 DR Interpro; IPR00380; Ppantne_attach.
 DR Pfam; PPF00550; PP-binding; 1.
 DR PRODOM; PD00887; Acyl_carrier; 1.
 DR TIGRFAMS; TIGR00317; Acyl_carrier; 1.
 DR PROSITE; PS0075; ACP_DOMAIN; 1.
 DR PROSITE; PS0012; PHOSPHOPANTETHINE; 1.
 KW Fatty acid biosynthesis; Phosphopantethine; chloroplast;
 KW transit peptide; Multigene family.
 FT TRANSIT 1 52 CHLOROPLAST (POTENTIAL).
 FT CHAIN 53 136 ACTYL CARRIER PROTEIN 1.
 FT BINDING 91 91 PHOSPHOPANTETHINE (BY SIMILARITY).
 SQ SEQUENCE 136 AA; 14351 MW; 8DF68F53079414FB CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Result 25
 Y4GB_RHISN STANDARD PRT; 139 AA.

DR EMBL; U88314; AAF99882.1; -.

DR WormPep; C46H11.3; CB08783; -.

SQ SEQUENCE 146 AA; 16843 MW; F6897C27F10D7A CRC64; -.

Query Match 3.2%; Score 6; DB 1; Length 146; -.

Best Local Similarity 100.0%; Pred. No. 62; -.

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; -.

QY 46 SADC GP 51

Db 26 SADC GP 31

RESULT 28

SSB_HUMAN STANDARD; PRT; 148 AA.

ID SSB_HUMAN

AC 004837;

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Single-stranded DNA-binding protein, mitochondrial precursor

DE (Mt-SSB) (MtSSB) (PW1P1-interacting protein 17).

GN SSBP1 OR SSBP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93246247; PubMed=8482537;

RA Tiranti V., Rocchi M., Didonato S., Zeviani M.;

RT Cloning of human and rat cDNAs encoding the mitochondrial single-stranded DNA-binding protein (SSB).";

RL Gene 126:219-225(1993).

RN [2]

RP SEQUENCE FROM N.A.

RA Honore B.;

RT "HPWP1-interacting protein 17 (ssDNA BP).";

RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Cervix;

RA straubberg R.;

RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 26-141.

RX MEDLINE=97185916; PubMed=9033597;

RA Yang C., Curth U., Urbanke C., Kang C.;

RT "Crystal structure of human mitochondrial single-stranded DNA binding protein at 2.4 Å resolution.";

RL Struct. Biol. 4:153-157(1997).

CC -i- FUNCTION: THIS PROTEIN BINDS PREFERENTIALLY AND COOPERATIVELY TO ss-DNA. PROBABLY INVOLVED IN MITOCHONDRIAL DNA REPLICATION.

CC -i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -i- SUBCELLULAR LOCATION: Mitochondrial.

CC -i- SIMILARITY: BELONGS TO THE SSB FAMILY.

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CC

DR EMBL; U67535; AAB98927.1; -.

DR TIGR; MJ0919; -.

KW HYPOTHETICAL PROTEIN; Complete proteome.

SQ SEQUENCE 149 AA; 16952 MW; 07B16483F957AE4 CRC64; -.

Query Match 3.2%; Score 6; DB 1; Length 149; -.

Best Local Similarity 100.0%; Pred. No. 63; -.

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; -.

QY 135 IEKLK 140

Db 120 IEKLK 125

RESULT 30

XYS2_PSEPU STANDARD; PRT; 157 AA.

DR Interpro; IPR000424; SSB_protein.

AC 005092;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE XYLDEGP operon transcriptional activator 2.
 GN XYL2.
 OS *Pseudomonas putida*.
 PL plasmid TOL PDK1, and Plasmid TOL pWW53.
 RC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN_HSI, and MT53;
 RX MEDLINE=9305221; PubMed=1331988;
 RA Assinder, S.J., de Marco P., Sayers J.R., Shaw L.E., Winson M.K.,
 RA Williams P.A.;
 RT "identical resolvases are encoded by *Pseudomonas* TOL plasmids pWW53
 and PDK1.";
 RL Nucleic Acids Res 20:5476-5476(1992).
 CC -1- FUNCTION: REGULATORY PROTEIN OF THE TOL PLASMID XYL OPERONS. XYLIS
 ACTIVATES THE XYLXZLTERFJKH OPERON REQUIRED FOR THE DEGRADATION
 OF TOLUENE, M-XYLENE AND P-XYLENE.
 CC -1- SUBCELLULAR LOCATION: cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ARAC/XYLIS FAMILY OF TRANSCRIPTIONAL
 REGULATORS.
 CC
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 CC
 CC EMBL; 1Q2642; AAAT1889.1; -.
 DR EML; 1Q2643; AAAT1891.1; -.
 DR S25486; S35486.
 DR PIR; S35488; S35488.
 DR InterPro; IPR00005; RTHARAC.
 DR Pfam; PF00165; RTH_ARAC; 2.
 DR PRINTS; PR00032; RTHARAC.
 DR SMART; SM0042; RTH_ARAC; 1.
 DR PROSITE; PS00041; RTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS01124; RTH_ARAC_FAMILY_2; 1.
 KW Aromatic hydrocarbons catabolism; Transcription regulation; Activator;
 KW DNA-binding; Plasmid.
 FT DNA_BIND 55 74 H-T-H MOTIF (BY SIMILARITY).
 SEQUENCE 157 AA: 17894 MN: A5FB035F3F8F674 CRC64;

Query Match 3.2%; Score 6; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 GFFHLG 169
 DR 115 GFFHLG 120

RN [1]

RESULT 31
 TEST_HUMAN ID TEI7_HUMAN STANDARD: PRT; 167 AA.
 AC 015273; (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE telethonin (titin cap protein).
 GN TCAP.
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=98010471; PubMed=9350988;
 RA Valle G., Faulkner G., de Antoni A., Pacchioni B., Pallavicini A.,
 Pandolfo D., Tiso N., Toppi S., Trevisan S., Ianfranchi G.;
 RT "Telethonin, a novel sarcomeric protein of heart and skeletal
 muscle.;"
 RL FEMS Lett. 415:163-168(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Palavicini A., Valle G., Lanfranchi G.;
 RA Palavicini A., Valle G., Lanfranchi G.;
 RT "Human telethonin genomic sequence.;"
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Mues A., Gauteil M.;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP INTERACTION WITH TITIN
 RX MEDLINE=98307394; PubMed=9645487;
 RA Mues A., van der Ven P.F., Young P., Furst D.O., Gauteil M.;
 RT "Two immunoglobulin-like domains of the Z-disc portion of titin
 interact in a conformation-dependent way with telethonin.";
 RL FEBS Lett. 428:111-114(1998).
 CC -1- SUBUNIT: INTERACTS WITH TITIN.
 CC -1- SUBCELLULAR LOCATION: SARCOMERIC.
 CC -1- TISSUE SPECIFICITY: HEART AND SKELETAL MUSCLE.
 CC -1- DISEASE: DEFECTS IN TCAP ARE A CAUSE OF LIMB-GIRDLE MUSCULAR
 DYSTROPHIES REPRESENT A GENETICALLY HETEROGENEOUS GROUP OF
 DISEASES WITH VARYING DEGREES OF SEVERITY DEPENDING ON AGE AT
 ONSET AND RATE OF PROGRESSION. THE FEATURE THAT ALL THESE
 CONDITIONS SHARE IS WEAKNESS STARTING IN THE PROXIMAL LIMB GIRDLE
 MUSCULATURE.
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 CC
 DR EMBL; AU00091; CAA04129.1; -.
 DR EMBL; AU01003; CAA08987.1; -.
 DR EMBL; AU011098; CAA09479.1; -.
 DR EMBL; BC012628; AAR12628.1; -.
 DR Genew; HGNC:11610; TCAP.
 DR MTM; 603488; -.
 DR MM; 601954; -.
 DR SEQUENCE 167 AA: 19052 MN: A3B0E27D8C84FF6C5 CRC64;

Query Match 3.2%; Score 6; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 TISTRP 73
 DR 29 TISTRP 34

RESULT 32
 TEST_MOUSE ID TEI7_MOUSE STANDARD: PRT; 167 AA.
 AC 070548; (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Telethonin (Titin cap protein).
 GN TCAP.
 OS Mus musculus (Mouse).
 OC BukaYvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Diaphragm;
 RA Levola C., Formentini E., Valle G., Ianfranchi G.,
 RT "Skeletal muscle transcripts characterization in Homo sapiens and Mus
 RT musculus.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Kolmerer B.;
 RT "The titin cap protein - a novel protein essential for sarcomere
 formation.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MUSCLE ASSEMBLY REGULATING FACTOR.
 CC -!- SUBUNIT: INTERACTS WITH TITIN.
 CC -!- SUBCELLULAR LOCATION: SARCOMERIC.
 CC
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 CC
 DR EMBL; AJ223854; CAB38077.1; -.
 DR MGD; MG1:133023; Tcap.
 SQ SEQUENCE 167 AA; 19078 MW; 2CB1F6F5415B4DC1 CRC64;
 Query Match 3.2%; Score 6; DB 1; Length 167;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 TLSTRP 73
 DR |||||
 Db 29 TLSTRP 34
 RESULT 33
 YC66_MESVI ID YC66_MESVI STANDARD; PRT; 170 AA.
 AC Q9M008;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 19.4 kDa protein YCF66 (Rf66).
 GN YCF66.
 OS Mesostigma viride.
 OC Chloroplast; Viridiplantae; Streptophyta; Mesostigmataceae;
 OC Mesostigmatales; Mesostigmataceae; Mesostigma.
 OC NCBI_TaxID=41882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIES-296;
 RX MEDLINE=20050907; PubMed=10688199;
 RA Lemieux C., Otis C., Turmel M.;
 RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
 branch of green plant evolution.";
 RL Nature 403:649-652(2000).
 CC -!- SIMILARITY: BELONGS TO THE YCF66 FAMILY.
 CC
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 CC
 DR EMBL; AE001202; AAC65190.1; -.
 DR HSSP; P02357; 1KRP.
 DR TIGR; TP0206; -
 DR InterPro; IPR000851; Ribosomal_S5.
 DR InterPro; IPR003324; Ribosomal_S5_C.
 DR Pfam; PF00333; Ribosomal_S5; 1.
 DR Pfam; PF03119; Ribosomal_S5_C; 1.
 DR TIGRFAMS; TIGR001021; rpsE_bact; 1.
 DR PROSITE; PS00585; RIBOSOMAL_S5; 1.
 DR Ribosomal protein; complete proteome.
 SQ SEQUENCE 172 AA; 18595 MW;
 Query Match 3.2%; Score 6; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -!- FUNCTION: DHPS CATALYZES THE FORMATION OF THE IMMEDIATE PRECURSOR OF FOLIC ACID. IT IS IMPLICATED IN RESISTANCE TO SULFONAMIDE.

CC -!- CATALYTIC ACTIVITY: 2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine diphosphate + 4-aminobenzoate = diphosphate + dihydrodopteroate.

CC -!- DHPS; diphosphate; biosynthesis; second step.

CC -!- SIMILARITY: TO OTHER SPECIES DHPS.

CC -----

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CC -----

CC EMBL; 104466; AA52083.1; -.

DR DR InterPro; IPR003579; GTPase_Rab.

DR DR InterPro; IPR001806; Ras_transfmrng.

DR DR InterPro; IPR005225; Small_GTP.

DR DR Pfam; PF00711; ras; 1.

DR DR PRINTS; PR00449; RASTRNSFRNG.

DR DR SMART; SM00175; RAB; 1.

DR DR TIGRFAMS; TIGR00331; small_GTP; 1.

DR DR GMP-binding; Lipoprotein; Prenylation.

FT FT NP-BIND 15 22 GTP (BY SIMILARITY).

FT FT NP-BIND 63 67 GTP (BY SIMILARITY).

FT FT NP-BIND 121 124 GTP (BY SIMILARITY).

FT FT DOMAIN 37 45 EFFECTOR_REGION (BY SIMILARITY).

FT FT LIPID 204 204 GERNYL-GERNYL (BY SIMILARITY).

FT FT Sequence 205 AA; 23192 MW; 2Bf51383A73724f1 CRC64;

FT -----

Query Match 3.2%; Score 6; DB 1; Length 205;

Best Local Similarity 100.0%; Pred. No. 84;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OX 182 SVOEGN 187

Db 172 SVOEGN 177

Query Match 3.2%; Score 6; DB 1; Length 205;

Best Local Similarity 100.0%; Pred. No. 84;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OX 182 SVOEGN 187

Db 172 SVOEGN 177

RESULT 38

RAB4_DICCDI STANDARD; PRT; 205 AA.

AC P36410; RAB4_DICCDI STANDARD; PRT; 205 AA.

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Rab-related protein Rab4.

DR RAB OR RAB4.

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

OC RAB4_TaxID=44689;

RN [1]

RP SEQUENCE FROM N.A.

RC SRR41-MSB/DSM 3109;

RX MEDLINE:99287316; Published:10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwynn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,

RA RT "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*.";

RT Nature 399:333-328(1995).

CC -----

CC -!- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.

CC -!- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE GUANYLATE KINASE FAMILY.

CC -----

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CC -----

CC EMBL; AE001809; AAD36756.1; -.

DR DR InterPro; IPR00619; Guanylate_kin.

DR DR Pfam; PF00628; GuKCK; 1.

DR DR PROSITE; PS00856; GUANYLATE_KINSE_1; 1.

DR DR PROSITE; PS50052; GUANYLATE_KINSE_2; 1.

DR DR Transferase; Kinase; APP-binding; Complete proteome.

FT KW_FT BIND 10 17 ATP (BY SIMILARITY).

CC -----

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CC -----

CC EMBL; U02927; AA80151.1; -.

DR DR dictypho; DD00069; rabd.

Query Match	3.2%; Score 6; DB 1; Length 207;	DE	Gene exporter protein B (Cytochrome c-type biogenesis protein ccmB).
Best Local Similarity	100.0%; Pred. No. 85;	GN	Paracoccus denitrificans.
Matches	6; Conservative 0; Mismatches 0;	OS	Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Qy	125 INEGKD 130	OC	Paracoccus.
Db	90 INEGKD 95	OX	NCBI_TaxID=266;
		RN	[1]
		RP	SEQUENCE FROM N.A.
		RC	STRAIN=Pd 1222;
		RX	MEDLINE=97195802; PubMed=9043133;
		RA	Page D., Pearce D.A., Norris H.A., Ferguson S.J.;
		RT	"The Paracoccus denitrifiers ccmA, B and C genes: cloning and sequencing, and analysis of the potential of their products to form a haem or apo-c-type cytochrome transporter.";
		RT	RL Microbiology 143:563-576(1997).
		CC	-!- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE
		CC	BIOGENESIS OF C-TYPE CYTOCHROMES (BY SIMILARITY).
		CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (Probable).
		CC	-!- SIMILARITY: BELONGS TO THE CCMB/CYW/HEB FAMILY.
		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
		CC	DR PRINTS; PR0314; CCMBBCMOGNIS.
		CC	DR TIGRFAMS; TIGR0190; CCMB; 1.
		CC	KW Cytochrome c-type biogenesis; transport; Transmembrane;
		FT	KW Inner membrane.
		FT	TRANSMEM 17 37 POTENTIAL.
		FT	TRANSMEM 47 67 POTENTIAL.
		FT	TRANSMEM 98 118 POTENTIAL.
		FT	TRANSMEM 125 145 POTENTIAL.
		FT	TRANSMEM 154 174 POTENTIAL.
		FT	TRANSMEM 190 210 POTENTIAL.
		SQ	SEQUENCE 215 AA; 21960 MW; 9882459B41E1D91 CRC64;
		DR	HSSP; P2181; IAM4.
		DR	InterPro; IPR003578; GTPase_Rho.
		DR	InterPro; IPR001805; Ras_transfmrng.
		DR	InterPro; IPR005225; Small_GTP.
		DR	Pfam; PF00071; ras; 1.
		DR	SMART; SM00174; RHO; 1.
		DR	TIGRFAMS; TIGR00231; small_GTP; 1.
		KW	GTP-binding.
		FT	NP_BIND 27 34 GTP (BY SIMILARITY).
		FT	NP_BIND 74 78 GTP (BY SIMILARITY).
		FT	NP_BIND 132 135 GTP (BY SIMILARITY).
		FT	DOMAIN 49 57 EFFECTOR_REGION (POTENTIAL).
		SQ	SEQUENCE 208 AA; 23220 MW; AF24D5821/17200F CRC64;
		Qy	172 DGSLDL 177
		Db	73 DGSLDL 78
			Query Match 3.2%; Score 6; DB 1; Length 215;
			Best Local Similarity 100.0%; Pred. No. 88;
			Matches 6; Conservative 0; Mismatches 0;
			Indels 0; Gaps 0;
			DE RAB14-related protein Rab-14.
			GN RAB14.
			OS Homo sapiens (Human), and
			OS Rattus norvegicus (Rat),
			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
			OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
			OX NCBI_TaxID=606, 10116;
		RN [1]	SEQUENCE FROM N.A.
		RP	SPCIES=Human; TISSUE=Liver;
		RA	Proikas-Cezanne T., Jenkins J.R.;
		RT	"Human Rab14 cloning and intracellular localization to the biosynthetic/secretory trafficking pathway";
		DT	15-JUN-2002 (Rel. 41, last annotation update)
			RESULT 41
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			DT 01-OCT-1996 (Rel. 34, .Created)
			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
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			AC P52219;
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			AC P52219;
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
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			AC P52219;
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
			CCMB_PARDE STANDARD; PRT; 215 AA.
			ID CCMB_PARDE STANDARD; PRT; 215 AA.
			AC P52219;
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
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			AC P52219;
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
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			AC P52219;
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
			CCMB_PARDE STANDARD; PRT; 215 AA.
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			AC P52219;
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
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			DT 01-OCT-1996 (Rel. 34, Last sequence update)
			DT 15-JUN-2002 (Rel. 41, last annotation update)
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			ID CCMB_PARDE STANDARD; PRT; 215 AA.
			AC P52219;
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KW Inner membrane.
 FT TRANSMEM 18 38 POTENTIAL.
 FT TRANSMEM 43 63 POTENTIAL.
 FT TRANSMEM 99 119 POTENTIAL.
 FT TRANSMEM 131 151 POTENTIAL.
 FT TRANSMEM 155 175 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 SQ SEQUENCE 218 AA; 22611 MW; CR2382RBD4B447F4 CRC64;

Query Match 3.2%; Score 6; DB 1; Length 218;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 DGSLDL 177
 Db 74 DGSLDL 79

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 AC Q00319; DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0008.
 GN MJ0008.
 OS Methanococcus jannaschii.
 OCHaeae; Euryarchaeota; Methanococci; Methanococcales;
 OCHaeae; Methanococcaceae; Methanococcaceae; Methanococcaceae; Methanococcaceae; Methanococcaceae; Methanococcaceae; NCBL-TaxID=2190;
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 RN STRAIN=ALL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkinis E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cottrell M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RL jannaschii.";
 CC SCIENCE 273:1058-1073(1996)
 CC " - FUNCTION: CULD BE INVOLVED IN NICKEL BINDING AND ACCUMULATION.
 CC -1- SIMILARITY: BELONGS TO THE HYPB/HUPM FAMILY.
 CC -----
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 CC -----
 DR U67495; AAB84429.1; -.
 DR TIGR; MJ00422; -.
 DR InterPro; IPR004392; HYPB.
 DR InterPro; IPR020294; HYPB_Ureg.
 DR Pfam; PF01405; HYPB_Ureg; 1.
 DR TIGRFAMs; TIGR00073; hypB; 1.
 KW Metal-binding; Nickel; Complete proteome.
 SQ SEQUENCE 221 AA; 24340 MW; OBB5415386a81138 CRC64;

Query Match 3.2%; Score 6; DB 1; Length 221;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 KMFELIE 136
 DR TIGR; MJ0008; -.
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Query Match 3.2%; Score 6; DB 1; Length 220;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 KMFELIE 198

RESULT 45
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AC Q07784;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable hydrogenase nickel incorporation protein hypB.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcaceae;
 OX NCBI_TaxID=2190;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=ALL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
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 RA Overbeek R., Kirkinis E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
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 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RL jannaschii.";
 CC SCIENCE 273:1058-1073(1996)
 CC " - FUNCTION: CULD BE INVOLVED IN NICKEL BINDING AND ACCUMULATION.
 CC -1- SIMILARITY: BELONGS TO THE HYPB/HUPM FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR U67495; AAB84429.1; -.
 DR TIGR; MJ00422; -.
 DR InterPro; IPR004392; HYPB.
 DR InterPro; IPR020294; HYPB_Ureg.
 DR Pfam; PF01405; HYPB_Ureg; 1.
 DR TIGRFAMs; TIGR00073; hypB; 1.
 KW Metal-binding; Nickel; Complete proteome.
 SQ SEQUENCE 221 AA; 24340 MW; OBB5415386a81138 CRC64;

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 Best Local Similarity 100.0%; Pred. No. 90;
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Qy 134 LIERKLI 139
 Db 49 LIERKLI 54

Search completed: November 9, 2002, 07:28:38
 Job time : 41 secs